W745

GNPAnnot: A Community Annotation System Applied To Sugarcane Sequences

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Room: Royal Palm Salon 1-2
Olivier Garsmeur , CIRAD, Montpellier, France
Gaetan Droc , CIRAD - UMR AGAP, Montpellier, France
Valentin Guignon , Bioversity International, Montpellier, France
Carine Charron , CIRAD, Montpellier, France
Angelique D'Hont , CIRAD, Montpellier, France
Manuel Ruiz , CIRAD, Montpellier, France
Stephanie Bocs , CIRAD, Montpellier, France
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A large amount of data is being produced by current genome sequencing projects. Sequence annotations need to be organized into databases and widely accessible. Like other species, sugarcane would benefit from centralized and innovative systems to study its genome. GNPAnnot is a community system performing structural and functional annotations of genes and allowing both automatic predictions and manual curations of genes and transposable elements (TEs). The system is currently being used for various plants, insect and fungus species. The GNPAnnot pipeline is made of a collection of programs that are connected together to automate genomic sequence annotations. Sequences and results are stored into the Chado GMOD database and can be visualized through a genome browser accessible from the Web portal of the SouthGreen bioinformatic platform (http://southgreen.cirad.fr/). Annotations can be manually edited using the Artemis genome editor. A database controller has been developed (Chado controller) in order to manage public and private annotation projects. It also provides an annotation history page for each gene or TE, and an annotation inspector that reports manual annotation mistakes. The GNPAnnot system is currently being used to annotate sugarcane BAC sequences in the framework of the SUGESI (Sugarcane Genome Sequencing Initiative) that aims at sequencing around 5,000 BACs, from cultivar R570, corresponding to the gene rich part of a monoploid genome of sugarcane.

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